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|-------------------|---|---|---------|---|-----|-------------------|--------------|--------------|---------------|---|--|---------------|-------------|--------|---|--|
| (a) | | double helix ; anti-parallel ; sugar-phosphate ; hydrogen ; | 4 | | | | | | | | | | | | | |
| (b) | (i) | percentages / amount , C & G similar (in all organisms) ; percentages / amount , A & T similar (in all organisms) ; different / named , organisms have different proportions of , bases / named base / AW ; greatest similarity between human and grasshopper ; least similarity between <i>E. coli</i> and the other three ; <i>E. coli</i> has similar proportions of all bases / <i>E. coli</i> has slightly more CG than AT / (named) eukaryote has more AT than CG ; comparative figs with units to support any statement ; | 3 max | mp 1 & 2 DO NOT CREDIT ref to a single organism mp 1 & 2 IGNORE ref to complementary DO NOT CREDIT statements in context of organism size e.g. statement that human has more A than <i>E. coli</i> / human has the most AT / <i>E. coli</i> has the most CG This mark is for a general statement e.g. human C = 19.8% and G = 19.9% human A = 30.9% and <i>E. coli</i> A = 24.7% 'human has more A (30.9%) than wheat (27.3%)' = 2 (mp 3 & 7) | | | | | | | | | | | | |
| (b) | (ii) | (suggests) A , bonds / pairs / links / connects / joins , to T ; (suggests) C , bonds / pairs / links / connects / joins , to G ; (suggests) purine bonds to pyrimidine ; (evidence for) complementary base pairing / which bases pair with each other / base pairing rules ; suggests bases point 'inwards' rather than 'outwards' ; | 2 max | IGNORE A – T or A = T unqualified IGNORE C – G or C = G unqualified ACCEPT 'bond' instead of 'pair' If a choice of answers is given, do not credit unless both answers are valid (e.g. two and double strands for DNA / ribose and pentose sugar) | | | | | | | | | | | | |
| (c) | Award 1 mark per correct row <table><tr><td>feature</td><td>DNA</td><td>RNA</td></tr><tr><td>number of strands</td><td>two / double</td><td>one / single</td></tr><tr><td>bases present</td><td>thymine / T (+ adenine + cytosine + guanine)</td><td>uracil / U (+ adenine + cytosine + guanine)</td></tr><tr><td>sugar present</td><td>deoxyribose</td><td>ribose</td></tr></table> | | feature | DNA | RNA | number of strands | two / double | one / single | bases present | thymine / T (+ adenine + cytosine + guanine) | uracil / U (+ adenine + cytosine + guanine) | sugar present | deoxyribose | ribose | 3 | ACCEPT letters instead of names of bases Names of bases must be unambiguous, so DO NOT CREDIT adenosine / thiamine / cysteine / etc. If more bases mentioned than T and U, then all bases must be included DO NOT CREDIT dioxynribose / oxynribose/ hexose / sugar IGNORE pentose |
| feature | DNA | RNA | | | | | | | | | | | | | | |
| number of strands | two / double | one / single | | | | | | | | | | | | | | |
| bases present | thymine / T (+ adenine + cytosine + guanine) | uracil / U (+ adenine + cytosine + guanine) | | | | | | | | | | | | | | |
| sugar present | deoxyribose | ribose | | | | | | | | | | | | | | |
| (d) | | carries / transfers, the (complementary DNA) , code / genetic information / copy of gene ; out of the nucleus ; (transfers it) to the, ribosome / RER / site of translation ; for, protein / polypeptide, synthesis ; | 2 max | IGNORE transcription DO NOT CREDIT ref to the whole DNA code / molecule ACCEPT 'to make protein' | | | | | | | | | | | | |
| Total | | | 14 | | | | | | | | | | | | | |

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| 2 | (a) | (i) | deoxyribose (sugar) ; phosphate (group) ; (nitrogenous / purine or pyrimidine) base / one correctly named base ; | 3 | DO NOT CREDIT dioxxyribose DO NOT CREDIT phosphate head or phosphate backbone DO NOT CREDIT letter instead of named base DO NOT CREDIT uracil DO NOT CREDIT incorrect spelling of thymine with 'a' |
| | (a) | (ii) | has ribose ; uracil / U, instead of, thymine / T ; single stranded ; 3 forms / AW ; | 2 max | assume answer refers to RNA unless otherwise stated DO NOT CREDIT incorrect spelling of thymine with 'a' |
| | (b) | 1 | untwist / unwind ; | 1 | DO NOT CREDIT unravel |
| | | S 2 S 3 | unzip / described ; H bond breaks ; | 2 | DO NOT CREDIT strands separating without qualification |
| | | 4 | both strands act as template ; | | |
| | | N 5 N 6 N 7 | (aligning of) free (DNA) nucleotides ; complementary, base / nucleotide, pairing ; C to G <u>and</u> T to A / purine to pyrimidine ; | 5 6 & 7 | DO NOT CREDIT bases Do not consider for QWC if mark awarded in the context of breaking apart or DNA structure only, rather than forming new double helix |
| | | R 8 R 9 R 10 | hydrogen bonds reform ; sugar-phosphate back bone forms ; (using) covalent / phosphodiester, bond ; | | |
| | | 11 12 13 | semi-conservative replication ; DNA polymerase ; AVP ; | 6 max | 12 CREDIT at any stage in the process 13 e.g. ligase / helicase / gyrase used in correct context C – G 3 H bonds / T – A 2 H bonds activation of free nucleotides (with 2 phosphates) synthesis in the 5' to 3' direction Okazaki fragments on lagging strand |
| | | | QWC - correct sequence – 1 S mark, then 1 N mark, then 1 R mark ; | 1 | It should be clear that candidate realises that the sequence is S, then N then R – even if not written in that order DO NOT CREDIT if any ref to transcription / translation DO NOT CREDIT 'codes for an amino acid' IGNORE enzyme / named protein |
| | (c) | (i) | polypeptide / protein / primary structure / a sequence of amino acids ; | 1 | |
| | (c) | (ii) | different, sequence of amino acids / primary structure / AW ; different protein / protein folds up differently / different tertiary structure ; (product) no longer functions / different function ; | 2 max | DO NOT CREDIT 'product' or incorrect biochemical (e.g. carbohydrate) ACCEPT suitable example, e.g. active site of enzyme no longer complimentary to substrate |
| Total | | | | 15 | |

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| 3 | (a) | (i) | | <p>Mark the first response but do not award the mark if a further answer is incorrect or contradictory DO NOT CREDIT refs to length as given in stem</p> <p>1 ACCEPT DNA is a double helix (as stranded is implied) for this mp DO NOT CREDIT DNA is a double <i>molecule</i></p> <p>2 ACCEPT (mRNA) not twisted / not coiled / not spiral / straight / ora</p> |
| | | | <p>1 (m)RNA is single stranded / DNA is double stranded ;</p> <p>2 (m)RNA is non helical / DNA is helical ;</p> | 1 |
| | (a) | (ii) | <p>1 RNA contains ribose and DNA contains deoxyribose ;</p> <p>2 RNA contains, uracil / U, and DNA contains, thymine / T ;</p> <p>3 3 / more than 1, forms of RNA ;</p> <p>4 RNA is, single <u>stranded</u> / non helical, and DNA is, double <u>stranded</u> / helical ; <i>if not already awarded as answer in (i)</i></p> | <p>Mark the first response to (a)(ii) – but but do not award the mark if a further answer is incorrect or contradictory</p> <p>2 DO NOT CREDIT thymine</p> <p>3 ACCEPT 'one form of DNA'</p> |
| | (a) | (iii) | gene ; | 1 |
| | (a) | (iv) | too big to / does not, fit through <u>pore</u> (in nuclear envelope) ; | 1 |
| | (a) | (v) | <p><i>idea that</i> only copies one, gene / section / part / AW, (of DNA) ;</p> <p><i>idea that</i> DNA comprises many, genes / alleles ;</p> | <p>e.g. mRNA only codes for 1 protein</p> <p>DO NOT CREDIT '1 DNA molecule contains <u>all</u> the genes' 'mRNA only codes for 1 protein but DNA codes for many proteins' = 2 marks</p> |

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|-------|-----|-------|---|----|--|
| 4 | (a) | (i) | <p>X cytosine / pyrimidine ;</p> <p>Y nucleotide ;</p> | 2 | <p>Mark the first answer on each prompt line. If the answer is correct and an additional answer is given that is incorrect or contradicts the correct answer then = 0 marks</p> <p>X ACCEPT <u>nitrogenous</u> base / <u>organic</u> base</p> <p>X IGNORE C</p> |
| | (a) | (ii) | <p>at least one line between all opposite bases ;</p> <p>two lines between A and T and three lines between both instances of C and G ;</p> | 2 | <p>IGNORE bond labels / H / O / δ^+ / δ^-</p> <p>Bases on left strand do not need to be labelled but CON this mark if incorrectly labelled</p> |
| | (a) | (iii) | <p>polypeptide ;</p> <p>ribosome ;</p> | 2 | <p>ACCEPT protein</p> |
| | (a) | (iv) | <p>(usually) single stranded / would not have 2 strands ;</p> <p>uracil / U, instead of thymine / T ;</p> | 2 | <p>Mark the first answer on each prompt line. If the answer is correct and an additional answer is given that is incorrect or contradicts the correct answer then = 0 marks</p> <p>IGNORE shorter</p> <p>ACCEPT only one backbone</p> <p>DO NOT CREDIT incorrect spelling of thymine with 'a'</p> <p>IGNORE difference in sugar as on the diagram ribose and deoxyribose would appear the same</p> |
| | (b) | (i) | <p><u>one</u> strand, from original DNA and <u>one</u> strand newly formed ;</p> <p>an , (original) strand / polynucleotide , acts as template (for new strand) ;</p> | 2 | <p>ACCEPT one old and one new strand</p> <p>ACCEPT each strand is copied</p> |
| | (b) | (ii) | <p>(DNA) can be replicated without error / same sequence of nucleotides is produced ;</p> <p>reduces occurrence of mutation ;</p> <p>allows (re-)formation of , hydrogen / H , bonds ;</p> | 2 | <p>ACCEPT formation of identical DNA</p> <p>ACCEPT same / correct , order / sequence , of bases</p> <p>This mark point is for the correct use of the term 'mutation' and does not imply without error.</p> <p>ACCEPT prevents mutation</p> <p>DO NOT CREDIT H⁺ / H₂ bonds</p> |
| | (c) | (i) | <p>horizontal band drawn in tube R1 clearly higher than band in ¹⁵N tube and clearly lower than band in ¹⁴N tube ;</p> | 1 | <p>DO NOT CREDIT if more than one band drawn</p> <p>IGNORE thickness of bands and whether bands are shaded</p> <p>DO NOT CREDIT if there is any overlap with a band in another tube</p> |
| | (c) | (ii) | <p>one band (in R2) clearly at the same height as that in tube R1 and one band (in R2) clearly at the same height as that in the ¹⁴N tube ;</p> | 1 | <div> </div> <p>DO NOT CREDIT if more than two bands drawn</p> <p>IGNORE thickness of bands and whether bands are shaded</p> |
| | (d) | | <p>same concentration of sugar (solution in each tube) ;</p> <p>same volume of, mixture / solution / sugar solution (in each tube) ;</p> <p>spin (all tubes) at same , speed / acceleration ;</p> <p>spin (all tubes) for same (length of) time ;</p> | 3 | <p>IGNORE prompt lines - mark as prose</p> <p>IGNORE amount throughout</p> <p>IGNORE mass</p> <p>IGNORE mass</p> <p>IGNORE volume , of sugar / DNA extract</p> <p>ACCEPT tubes spun at constant speed</p> <p>IGNORE temperature / pH</p> <p>IGNORE mass of DNA</p> |
| Total | | | | 17 | |